

#17
DmT
11-7-02

RAW SEQUENCE LISTING

DATE: 11/04/2002

PATENT APPLICATION: US/09/721,456

TIME: 16:18:10

Input Set : N:\Crf3\RULE60\09721456.raw

Output Set: N:\CRF4\11042002\I721456.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Cech, Thomas R.

6 Lingner, Joachim

7 Nakamura, Toru

8 Chapman, Karen B.

9 Morin, Gregg B.

10 Harley, Calvin B.

11 Andrews, William H.

13 (ii) TITLE OF INVENTION: Human Telomerase Catalytic Subunit

15 (iii) NUMBER OF SEQUENCES: 727

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

19 (B) STREET: Two Embarcadero Center, Eighth Floor

20 (C) CITY: San Francisco

21 (D) STATE: California

22 (E) COUNTRY: USA

23 (F) ZIP: 94111-3834

ENTERED

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/721,456

C--> 33 (B) FILING DATE: 22-Nov-2000

34 (C) CLASSIFICATION:

76 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/974,549A

38 (B) FILING DATE: 19-NOV-1997

41 (A) APPLICATION NUMBER: US 08/724,643

42 (B) FILING DATE: 01-OCT-1996

45 (A) APPLICATION NUMBER: US 08/844,419

46 (B) FILING DATE: 18-APR-1997

49 (A) APPLICATION NUMBER: US 08/846,017

50 (B) FILING DATE: 25-APR-1997

53 (A) APPLICATION NUMBER: US 08/851,843

54 (B) FILING DATE: 06-MAY-1997

57 (A) APPLICATION NUMBER: US 08/854,050

58 (B) FILING DATE: 09-MAY-1997

61 (A) APPLICATION NUMBER: US 08/911,312

62 (B) FILING DATE: 14-AUG-1997

65 (A) APPLICATION NUMBER: US 08/912,951

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66      (B) FILING DATE: 14-AUG-1997
69      (A) APPLICATION NUMBER: US 08/915,503
70      (B) FILING DATE: 14-AUG-1997
73      (A) APPLICATION NUMBER: WO PCT/US97/17618
74      (B) FILING DATE: 01-OCT-1997
77      (A) APPLICATION NUMBER: WO PCT/US97/17885
78      (B) FILING DATE: 01-OCT-1997
80      (viii) ATTORNEY/AGENT INFORMATION:
81          (A) NAME: Apple, Randolph Ted
82          (B) REGISTRATION NUMBER: 36,429
83          (C) REFERENCE/DOCKET NUMBER: 015389-002610US
85      (ix) TELECOMMUNICATION INFORMATION:
86          (A) TELEPHONE: (415) 576-0200
87          (B) TELEFAX: (415) 576-0300
90      (2) INFORMATION FOR SEQ ID NO: 1:
92          (i) SEQUENCE CHARACTERISTICS:
93              (A) LENGTH: 4015 base pairs
94              (B) TYPE: nucleic acid
95              (C) STRANDEDNESS: single
96              (D) TOPOLOGY: linear
98          (ii) MOLECULE TYPE: cDNA
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102             (A) NAME/KEY: CDS
103             (B) LOCATION: 56..3454
104             (D) OTHER INFORMATION: /product= "hTRT"
105 /note= "human telomerase reverse
106 transcriptase (hTRT) catalytic protein
107 component"
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112 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG      58
113                                     Met
114                                     1
116 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC      106
117 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
118           5              10              15
120 TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC      154
121 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
122           20              25              30
124 CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG      202
125 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
126           35              40              45
128 CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC      250
129 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
130           50              55              60              65
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133 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
134           70              75              80
136 GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG      346
137 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu

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141	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp
142		100				105		
144	GCC	TTC	ACC	ACC	AGC	GTG	CGC	TAC
145	Ala	Phe	Thr	Thr	Ser	Val	Arg	Tyr
146		115				120		
148	GCA	CTG	CGG	GGG	AGC	GGG	GCG	TGG
149	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp
150	130					135		
152	GAC	GAC	GTG	CTG	GTT	CAC	CTG	CTG
153	Asp	Asp	Val	Leu	Val	His	Leu	Leu
154						150		
156	GTG	GCT	CCC	AGC	TGC	GCC	TAC	CAG
157	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln
158						165		
160	CTC	GGC	GCT	GCC	ACT	CAG	GCC	CGG
161	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg
162						180		
164	CGA	AGG	CGT	CTG	GGA	TGC	GAA	CGG
165	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg
166						200		
168	GCC	GGG	GTC	CCC	CTG	GGC	CTG	CCA
169	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro
170	210					215		
172	GGC	AGT	GCC	AGC	CGA	AGT	CTG	CCG
173	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro
174						230		
176	GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG
177	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr
178						245		
180	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG
181	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro
182						260		
184	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA
185	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu
186						275		
188	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA
189	Ser	Gly	Thr	Arg	His	Ser	His	Pro
190	290					295		
192	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA
193	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro
194						310		
196	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG
197	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys
198						325		
200	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC
201	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe
202						340		

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204	CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG	GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	1162
205	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	
206		355					360					365					
208	CCC	TGG	ATG	CCA	GGG	ACT	CCC	CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	1210
209	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	
210	370					375				380					385		
212	TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
213	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
214				390						395					400		
216	CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
217	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
218			405						410					415			
220	GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
221	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
222			420					425						430			
224	TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
225	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
226		435					440					445					
228	CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
229	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
230	450					455					460					465	
232	CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
233	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
234				470						475					480		
236	CAC	AAC	GAA	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG		1546
237	His	Asn	Glu	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu		
238			485						490					495			
240	GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
241	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
242			500					505						510			
244	GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
245	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
246		515						520						525			
248	CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
249	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
250	530					535					540					545	
252	CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
253	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
254				550						555					560		
256	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
257	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
258			565						570					575			
260	AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
261	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
262			580						585					590			
264	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
265	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
266		595					600							605			
268	CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930

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269	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
270	610					615					620					625	
272	AAG	CCT	GAC	GGG	CTG	CGG	CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	1978
273	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	
274				630						635						640	
276	GCC	AGA	ACG	TTC	CGC	AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	2026
277	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	
278				645					650					655			
280	GTG	AAG	GCA	CTG	TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	2074
281	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	
282			660					665					670				
284	GGC	CTC	CTG	GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	2122
285	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	
286		675					680				685						
288	TGG	CGC	ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	2170
289	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	
290	690					695				700						705	
292	CTG	TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC	2218
293	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	
294				710					715						720		
296	CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG	AAC	2266
297	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	
298			725					730					735				
300	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC	CAT	GGG	2314
301	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
302			740					745					750				
304	CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	TCT	ACC	TTG	ACA	GAC	CTC	2362
305	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	
306		755				760					765						
308	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	GAG	ACC	AGC	CCG	2410
309	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	
310	770					775					780					785	
312	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	TCC	CTG	AAT	GAG	GCC	2458
313	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
314				790					795					800			
316	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	TTC	ATG	TGC	CAC	CAC	GCC	2506
317	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
318			805					810					815				
320	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	CAG	TGC	CAG	GGG	ATC	CCG	CAG	2554
321	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
322			820					825					830				
324	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	2602
325	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
326		835					840					845					
328	GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	2650
329	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
330	850					855				860						865	
332	TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	2698
333	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/721,456DATE: 11/04/2002
TIME: 16:18:11Input Set : N:\Crf3\RULE60\09721456.raw
Output Set: N:\CRF4\11042002\I721456.raw

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Seq#:534; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:534; N Pos. 23,24,25,26,27,28,29,30
Seq#:535; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:535; N Pos. 23,24,25,26,27,28,29,30
Seq#:536; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:536; N Pos. 23,24,25,26,27,28,29,30
Seq#:538; N Pos. 16
Seq#:540; Xaa Pos.2,4
Seq#:556; N Pos. 1,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26
Seq#:569; N Pos. 16
Seq#:571; N Pos. 1,2,3,6
Seq#:574; N Pos. 7,10
Seq#:575; N Pos. 1,16,17,18,21
Seq#:576; N Pos. 9,12
Seq#:577; Xaa Pos.5
Seq#:578; N Pos. 9,12,15,18
Seq#:579; Xaa Pos.2,3
Seq#:580; N Pos. 9,15
Seq#:582; N Pos. 15
Seq#:594; N Pos. 1
Seq#:633; Xaa Pos.1,3,4

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Output Set: N:\CRF4\11042002\I721456.raw

Seq#:634; Xaa Pos.1,3,5,6,7
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Seq#:636; Xaa Pos.2,4,6,7,14,17,18
Seq#:637; Xaa Pos.5,8,10
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Seq#:727; Xaa Pos.23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41
Seq#:727; Xaa Pos.42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60
Seq#:727; Xaa Pos.61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79
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Seq#:727; Xaa Pos.670,671,672,673,674,675,676,677,678,679,680,681,682,683
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Seq#:727; Xaa Pos.731,732,733,734,735,736,737,738,739,740,741,742,743,744
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Seq#:727; Xaa Pos.759,760,761,762,763,764,765,766,767,768,769,770,771,772
Seq#:727; Xaa Pos.773,774,775,776,777,778,779,780,781,782,783,784,785,786
Seq#:727; Xaa Pos.787,788,789,790,791,792,793,794,796,797,798,800,801,802
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Seq#:727; Xaa Pos.833,834,835,836,837,838,839,840,841,842,843,844,845,846
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Seq#:727; Xaa Pos.964,965,966,967,968,969,970,971,972,973,974,975,976,977
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Seq#:727; Xaa Pos.992,993,994,995,996,997,998,999,1000,1003,1005,1006,1007
Seq#:727; Xaa Pos.1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018
Seq#:727; Xaa Pos.1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029
Seq#:727; Xaa Pos.1030,1031,1032,1033,1034,1035,1036,1037,1038,1039

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Input Set : N:\Crf3\RULE60\09721456.raw

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:660 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:765 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1215 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1444 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1473 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:1591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32
L:1650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16
L:1656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:32
L:1931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:1971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:2003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:2042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:2170 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:2345 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:2518 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:2721 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:2875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:2923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:2941 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:3151 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:3353 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:4246 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:4395 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=105
L:4423 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:4417 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=106
L:4446 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:4440 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=107
L:4468 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:4468 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=108
L:4462 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=108
L:4491 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:5081 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 111
L:5209 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 111
L:5305 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 111
L:5586 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=114
L:7976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:195 after pos.:0
L:8008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:196 after pos.:0
L:8056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:197 after pos.:0
L:8096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:198 after pos.:0
L:8152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:0
L:8565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:214 after pos.:0
L:10092 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=238

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L:10142 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=241
L:10376 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:10518 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:10661 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:10895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:267 after pos.:96
L:11804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:64
L:11807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:80
L:11810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:96
L:11813 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:112
L:11822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:160
L:11825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:176
L:11828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:192
L:11831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:208
L:11889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295 after pos.:64
L:11908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:296 after pos.:0
L:11911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:296 after pos.:16
L:12107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304 after pos.:0
L:12480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:64
L:12483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:80
L:12486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:96
L:12498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:160
L:12501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:176
L:12507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 after pos.:208
L:12548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:322 after pos.:128
L:12551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:322 after pos.:144
L:12674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:325 after pos.:64
L:12927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:334 after pos.:64
L:12930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:334 after pos.:80
L:12947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:335 after pos.:0
L:12950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:335 after pos.:16
L:12975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336 after pos.:16
L:12978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336 after pos.:32
L:12981 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336 after pos.:48
L:12984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336 after pos.:64
L:13011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336 after pos.:208
L:14382 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=362
L:14398 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=363
L:14431 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=365
L:14447 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=366
L:14480 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=368
L:14496 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=369
L:14529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=371
L:14545 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=372
L:14578 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=374
L:14611 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=376
L:14627 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=377
L:14649 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=378
L:14671 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=379
L:14693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=380

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L:14721 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:14715 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=381
L:14737 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=382
L:14759 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=383
L:14781 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=384
L:14803 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=385
L:14825 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=386
L:14847 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=387
L:14869 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=388
L:14891 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=389
L:14919 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:14913 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=390
L:14935 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=391
L:14957 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=392
L:14979 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=393
L:15001 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=394
L:15029 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15023 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=395
L:15051 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15045 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=396
L:15073 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15067 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=397
L:15095 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15089 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=398
L:15117 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15111 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=399
L:15139 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15133 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=400
L:15161 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15155 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=401
L:15183 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15177 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=402
L:15205 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15199 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=403
L:15221 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=404
L:15249 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15243 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=405
L:15265 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=406
L:15287 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=407
L:15309 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=408
L:15469 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15689 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:15909 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16085 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16261 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16349 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16621 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16643 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16665 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/721,456

DATE: 11/04/2002

TIME: 16:18:11

Input Set : N:\Crf3\RULE60\09721456.raw

Output Set: N:\CRF4\11042002\I721456.raw

L:16687 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16731 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16819 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16885 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:16973 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:17241 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:17351 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]

Application No.: 09721458

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

APPLICANT IS GIVEN ONE EXTENDIBLE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to _____ whose telephone number is (703) 30 _____



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Application No.: 09721456

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
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The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

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